

Amendments to the Specification

Please replace the paragraph beginning at page 32, line 3, with the following amended paragraph.

The structure coordinates set forth in Figure 4 can be used to aid in obtaining structural information about another crystallized molecule or molecular complex. The method of the invention allows determination of at least a portion of the three-dimensional structure of molecules or molecular complexes which contain one or more structural features that are similar to structural features of *S. aureus* MurB. These molecules are referred to herein as "structurally homologous" to *S. aureus* MurB. Similar structural features can include, for example, regions of amino acid identity, conserved active site or binding site motifs, and similarly arranged secondary structural elements (e.g., α helices and β sheets). Optionally, structural homology is determined by aligning the residues of the two amino acid sequences to optimize the number of identical amino acids along the lengths of their sequences; gaps in either or both sequences are permitted in making the alignment in order to optimize the number of identical amino acids, although the amino acids in each sequence must nonetheless remain in their proper order. Preferably, two amino acid sequences are compared using the Blastp program, version 2.0.9, of the BLAST 2 search algorithm, as described by Tatusova et al., FEMS Microbiol Lett 174, 247-50 (1999), and available on the world wide web at ncbi.nlm.nih.gov/gorf/bl2.html ~~http://www.ncbi.nlm.nih.gov/gorf/bl2.html~~. Preferably, the default values for all BLAST 2 search parameters are used, including matrix = BLOSUM62; open gap penalty = 11, extension gap penalty = 1, gap x_dropoff = 50, expect = 10, wordsize = 3, and filter on. In the comparison of two amino acid sequences using the BLAST search algorithm, structural similarity is referred to as "identity." Preferably, a structurally homologous molecule is a protein that has an amino acid sequence sharing at least 65% identity with a native or recombinant amino acid sequence of *S. aureus* MurB (for example, SEQ ID NO:1). More preferably, a protein that is structurally homologous to *S. aureus* MurB includes at least one contiguous stretch of at least 50 amino acids

Serial No.: 09/991,211

Confirmation No.: 4477

Filed: November 21, 2001

For: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF STAPHYLOCOCCUS AUREUS UDP-N-ACETYLENOLPYRUVYLGLUCOSAMINE REDUCTASE (S. aureus MurB)

that shares at least 80% amino acid sequence identity with the analogous portion of the native or recombinant *S. aureus* MurB (for example, SEQ ID NO:1). Methods for generating structural information about the structurally homologous molecule or molecular complex are well-known and include, for example, molecular replacement techniques.